Amendments to the Specification:

Please **delete** the paragraph on page 3, line 14 through page 5, line 24, and **replace it** with the following paragraph entitled "Description of the Figures".

DESCRIPTION OF THE FIGURES

Figure 1. DNA **(SEQ ID NO: 1)** and translated amino acid sequence **(SEQ ID NO: 2)** of *Cuphea hookeriana* KAS factor B clone chKAS B-2 are provided.

Figure 2. DNA **(SEQ ID NO: 3)** and translated amino acid sequence **(SEQ ID NO: 4)** of *Cuphea hookeriana* KAS factor B clone chKAS B-31-7 are provided.

Figure 3. DNA **(SEQ ID NO: 5)** and translated amino acid sequence **(SEQ ID NO: 6)** of *Cuphea hookeriana* KAS factor A clone chKAS A-2-7 are provided.

Figure 4. DNA **(SEQ ID NO: 7)** and translated amino acid sequence **(SEQ ID NO: 8)** of *Cuphea hookeriana* KAS factor A clone chKAS A-1-6 are provided.

Figure 5. DNA **(SEQ ID NO: 9)** and translated amino acid sequence **(SEQ ID NO: 10)** of *Cuphea pullcherrima* KAS factor B clone cpuKAS B/7-8 are provided.

Figure 6. DNA **(SEQ ID NO: 11)** and translated amino acid sequence **(SEQ ID NO: 12)** of *Cuphea pullcherrima* KAS factor B clone cpuKAS B/8-7A are provided.

Figure 7. DNA **(SEQ ID NO: 13)** and translated amino acid sequence **(SEQ ID NO: 14)** of *Cuphea pullcherrima* KAS factor A clone cpuKAS A/p7-6A are provided.

Figure 8. Preliminary DNA sequence **(SEQ ID NO: 15)** of *Cuphea pullcherrima* KAS factor A clone cpuKAS A/p8-9A is provided.

Figure 9. DNA **(SEQ ID NO: 16)** and translated amino acid sequence **(SEQ ID NO: 17)** of *Cuphea hookeriana* KASIII clone chKASIII-27 are provided.

Figure 10. The activity profile for purified cpuKAS B/8-7A using various acyl-ACP substrates is provided.

Figure 11. The activity profile for purified chKAS A-2-7 and chKAS A-1-6 using various acyl-ACP substrates is provided.

Figure 12. The activity profile for purified castor KAS factor A using various acyl-ACP substrates is provided.

Figure 13. The activity profile for purified castor KAS factor B using various acyl-ACP substrates is provided.

Figure 14. A graph showing the number of plants arranged according to C8:0 content for transgenic plants containing CpFatB1 versus transgenic plants containing CpFatB1 + chKAS A-2-7 is provided.

Figure 15**A**. ~~Graphs~~ **Graph** showing the %C10/%C8 ~~ratios~~ **ratio** in transgenic plants **resulting from cross of plants** containing ChFatB2 (4804-22-357) and ~~in plants resulting from crosses between 4804-22-357 and~~ 5401-9 (chKAS A-2-7 plants) ~~are~~ **is** provided.

Figure 15B. Graph showing the %C10/%C8 ratio in transgenic plants containing ChFatB2 (4804-22-357) is provided.

Figure 16**A**. ~~Graphs~~ **Graph** showing the %C10 + %C8 ~~contents~~ **content** in transgenic plants **resulting from cross of plants** containing ChFatB2 (4804-22-357) and ~~in plants resulting from crosses between 4804-22-357 and~~ 5401-9 (chKAS A-2-7 plants) ~~are~~ **is** provided.

Figure 16B. Graph showing the %C10 + %C8 content in transgenic plants containing ChFatB2 (4804-22-357) is provided.

Figure 17**A**. ~~Graphs~~ **Graph** showing the %C10/%C8 ~~ratios~~ **ratio** in transgenic plants **resulting from cross of plants** containing ChFatB2 (4804-22-357) and ~~in plants resulting from crosses between 4804-22-357 and~~ 5413-17 (chKAS A-2-7 + CpFatB1 plants) ~~are~~ **is** provided.

Figure 17B. Graph showing the %C10/%C8 ratio in transgenic plants containing ChFatB2 (4804-22-357) is provided.

Figure 18**A**. ~~Graphs~~ **Graph** showing the %C10 + %C8 ~~contents~~ **content** in transgenic plants

resulting from cross of plants containing ChFatB2 (4804-22-357) ~~and in plants resulting from crosses between 4804-22-357~~ and 5413-17 (chKAS A-2-7 + CpFatB1 plants) ~~are~~ **is** provided.

Figure 18B. Graph showing the %C10 + %C8 content in transgenic plants containing ChFatB2 (4804-22-357) is provided.

Figure 19**A**. ~~Graphs~~ **Graph** showing the %C12:0 in transgenic plants containing Uc FatB1 (LA86DH186) ~~and in plants resulting from crosses with wild type (X WT) and with lines expressing Ch KAS A-2-7~~ **is provided.**

Figure 19B. Graph showing the %C12:0 in transgenic plants resulting from cross of plants containing Uc FatB1 (LA86DH186) and wild type (X WT) is provided.

Figure 19C. Graph showing the %C12:0 in transgenic plants resulting from cross of plants containing Uc FatB1 (LA86DH186) and lines expressing Ch KAS A-2-7 is provided.

Figure 20. Graph showing the relative proportions of C12:0 and C14:0 fatty acids in the seeds of transgenic plants containing Uc FatB1 (LA86DH186) and in plants resulting from crosses with wild type (X WT) and with lines expressing Ch KAS A-2-7.

Figure 21**A**. ~~Graphs~~ **Graph** showing the %C18:0 in transgenic plants containing Garm FatB1 (5266) ~~and in seeds of plants resulting from crosses with wild type (X WT) and with lines expressing Ch KAS A-2-7~~ **is provided.**

Figure 21B. Graph showing the %C18:0 in transgenic seeds resulting from cross of plants containing Garm FatB1 (5266) and wild type (X WT) is provided.

Figure 21C. Graph showing the %C18:0 in transgenic seeds of plants resulting from cross of plants containing Garm FatB1 (5266) and lines expressing Ch KAS A-2-7 is provided.

Figure 22. The activity profile of Ch KAS A in protein extracts from transgenic plants containing Ch KAS A-2-7. Extracts were preptreated with the indicated concentrations of cerulenin.

Please **delete** the paragraph on page 24, line 12-25, and **replace it** with the following paragraph:

Fatty acid analysis of several events resulting from the crosses between transgenic lines containing ChFatB2 (4804-22-357) and chKAS A-2-7 (5401-9), reveal an increase in the ratio of C:10/C:8 levels (~~Figure 15~~**Figures 15A and 15B**). This C:10/C:8 ratio in nearly all of the transgenic events containing ChFatB2 TE alone fluctuates between 3 and 6, whereas in the F1 generation of transgenic containing both the TE and the KAS A-2-7, the ratio can be as high as 22. This increase in C:10 levels is accompanied by an increase in the total C:8 and C:10 content (~~Figure 16~~**Figures 16A and 16B**). The sum of the C:8 and C:10 fatty acids in the heterozygous F1 lines is as high as those in the homozygous parent line (4804-22-357), whereas the heterozygous lines usually contain substantially less C:8 and C:10 than the homozygous lines.

Please **delete** the paragraph on page 24, line 26 through page 25, line16, and **replace it** with the following paragraph:

Similar results were observed in F1 generation seeds resulting from crosses performed between 4804-22-357 (ChFatB2) and the 5413-17 event (CpFatB1 and chKAS A-2-7 tandem). Levels of C:8 and C:10 in the 5413-17 line were 6.3 and 2.8 mol% respectively. Data presented in ~~Figure 17~~ **Figures 17A and 17B** show that there is shift towards C:10 fatty acids as was observed with the 4804-22-357 (ChFatB2) x 5401-9 (chKAS A-2-7) crosses. Furthermore, ~~Figure 18~~ **Figures 18A and 18B** indicates the presence of two separate populations of heterozygotes. Those containing approximately 9-11 weight percent C:10 + C:8 are believed to represent offspring containing a single copy of the ChFatB1 TE gene and

no copies of the CpFatB1 and chKAS A genes from 5413. Those plants containing approximately 15-20 weight percent C:10 + C:8 are believed to represent the heterozygotes containing a single ChFatB1 TE gene as well as the CpFatB1 and chKAS A genes from 5413. Thus, the level of the C:10 + C:8 fatty acids does not decrease to 50% of that detected in parent lines when a copy of the ChKAS A gene is present.

Please **delete** the paragraph on page 26, line 1 through line 13, and **replace it** with the following paragraph:

However, crosses between LA86DH186 and the 5401-9 hemizygous line led to an accumulation of up to 57 mol% C12:0 in the seed oil of F1 progeny (~~Figure 19~~**Figures 19A, 19B, and 19C**). Interestingly, in crosses with LA86DH186 x untransformed control line and LA86DH186 x 5401-9, levels of C14:0 in the seeds of the F1 progeny decreased to 50% of the levels obtained in homozygous LA86DH186 lines (Figure 20). Furthermore, increases in the proportion of C12:0 fatty acid resulted in a substantial decline in the proportions of all the long-chain fatty acyl groups (C16:0, C18:0, C18:2, and C18:3). These results indicate that the ChKAS A-2-7 is an enzyme with substrate specificity ranging from C6:0 to C10:0-ACP, and that its over-expression ultimately reduces the longer chain acyl-ACP pools.

Please **delete** the paragraph on page 26, line 14 through line 24, and **replace it** with the following paragraph:

Further evidence is obtained in support of the chain length specificity of the ChKAS A-2-7 in crosses of the 5401-9 line with a transgenic line (5266) expressing an 18:1/18:0 TE from *Garcinia mangostana* (GarmFatA1, US patent application No. 08/440,845). Transgenic *Brassica* line 5266 has been shown to accumulate up to 24 mol% C18:0 in the seed oil of homozygous lines (~~Figure 21~~ **Figures 21A, 21B, and 21C**). However, in the seed oil of F1 progeny of crosses between 5266 and 5401-9 levels of C18:0 were reduced to approximately 12 mol%. Furthermore, levels of C16:0 generated from these crosses was similar to the levels obtained from the seed oil of nontransgenic control plants.